

FIGURE 1**RTVP and RGL1 α , RGL1 β DNA compare**

RTVP-1	1	CTCTGTTTTCTCAAAGCTGAAGTCGGCTAGGTTTGCAAAGCTGTGGGCTG
RGL α	1	-----
RGL β	1	-----
consensus	1	-----
RTVP-1	51	AGCACTCAGGCAATCACACTCTCAGAACTGCGGCGGCTCTGGACTGCAG
RGL α	1	-----CATCCTCCGCATC-CTCCAC---AT
RGL β	1	-----CATCCTCCGCATC-CTCCAC---AT
consensus	51	cAtCctCcGCatC CTccAC At
RTVP-1	101	CCTCCCAAGGCTCCATGCCAGACAAAGCATGCGTGTCACACTTGCTACAA
RGL α	22	CCTTCCATGGCTC--TG-----AAGAATAAATT---CAGTTGTTTATG
RGL β	22	CCTTCCATGGCTC--TG-----AAGAATAAATT---CAGTTGTTTATG
consensus	101	CCTtCCAtGGCTC TG AAGaATAaaTt CAgTTGtTtatg
RTVP-1	151	TAGCCTGGATGGTTTCTTTTGTCTCCAATTATTCACACACAGCAAATATT
RGL α	60	GATCTTGGGTC-TGTGTTTGGTAGCCACTACATCTTCCA----AAATC--
RGL β	60	GATCTTGGGTC-TGTGTTTGGTAGCCACTACATCTTCCA----AAATC--
consensus	151	gAtCtTGGgTc TgTgTTTgGTagCCAcTacaTcttcca AAATc
RTVP-1	201	TTGCCAGATATCGAAAATGAAGATTTTCATCAAAGACTGCGTTTCGAATCCA
RGL α	103	---CCATCCATCACTGACCCACACTTTTATAGACAACCTGCATAGAAGCCCA
RGL β	103	---CCATCCATCACTGACCCACACTTTTATAGACAACCTGCATAGAAGCCCA
consensus	201	CCAtccATCactgAcCCAcAcTtTtATagAcaACTGCaTagaAgcCCA
RTVP-1	251	TAACAAGTTCCGATCAGAGGTGAAACCAACAGCCAGTGATATGCTATACA
RGL α	150	CAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACA
RGL β	150	CAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACA
consensus	251	cAACgAaTggCGtgggcaAaGTcAAcCctcCcGCggccGAcATGaaATACA
RTVP-1	301	TGACTTGGGACCCAGCACTAGCCCAAATTGCAAAAGCATGGGCCAGCAAT
RGL α	200	TGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAG
RGL β	200	TGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAG
consensus	301	TGAtTTGGGataaaAGgttTAGCaaAgATgGctAAAGCATGGGCaAaCcAg
RTVP-1	351	TGCCAGTTTTTCACATAATACACGGCTGAAGCCACCCCAAGCTGC-ACC
RGL α	250	TGCAAATTTGAACATAATGACTGTTTGGATAAATCATATAAA-TGCTATG
RGL β	250	TGCAAATTTGAACATAATGACTGTTTGGATAAATCATATAAA-TGCTATG
consensus	351	TGCaAaTTTgaACATAATgactGttTGgAtaaAtCatAtAaa TGctAtg
RTVP-1	400	CAAACCTTCACTTCACTGGGAGAGAACATCTGGACTGG--GTCTGTGCCCA
RGL α	299	CAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGTGGAATAAAGTCA
RGL β	299	CAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGTGGAATAAAGTCA

consensus 401 CAgctTTtgaaTatgTtGGAGAAaAtATCTGGttaGGtgGaaTaaagtCA

RTVP-1 448 TTTTTTCTGTGTCTTCCGCCATCACAAACTGGTATGACGAAATCCAGGAC
 RGL α 349 TTCACACCAAGACAT--GCCATTACGGCTTGGTATAATGAAACCCAATTT
 RGL β 349 TTCACACCAAGACAT--GCCATTACGGCTTGGTATAATGAAACCCAATTT
 consensus 451 TTcacaCcaaGaCaT GCCATtACggctTGGTATaAtGAAacCCAattt

RTVP-1 498 TATGACTTCAAGACTCGGATATGCAAAAAAGTCTGTGGCCACTACACTCA
 RGL α 397 TATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACA
 RGL β 397 TATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACA
 consensus 501 TATGAtTTtgAtAgTctatcATGctccAgAGTCTGTGGCCAtTAtACaCa

RTVP-1 548 GGTTGTTTGGGCAGATAGTTACAAAGTTGGCTGCGCAGTTCAATTTTGCC
 RGL α 447 GTTAGTTTGGGCCAATTCATTTTATGTCTGGTGTGCAGTTGCAATGTGTC
 RGL β 447 GTTAGTTTGGGCCAATTCATTTTATGTCTGGTGTGCAGTTGCAATGTGTC
 consensus 551 GtTaGTTTGGGCcaATtcaTtttAtGTcGGtTgtGCAGTTgcAaTgTGtC

RTVP-1 598 CTAAAGTTTCTGGCTTTGACGCTCTTTCCAATGGAGCACATTTTATATGC
 RGL α 497 CTAA-----CCTTGGGGGAGCTTCAACTGCAATA---TTTGTATGC
 RGL β 497 CTAA-----CCTTGGGGGAGCTTCAACTGCAATA---TTTGTATGC
 consensus 601 CTAA CcTTGggGgagcTTCaAcTGcAaTA TTTgtATGC

RTVP-1 648 AACTACGGACCAGGAGGGAATTACCCAACCTGGCCATATAA---GAGAGG
 RGL α 535 AACTACGGACCTGCAGGAAATTTTGCAAATATGCCTCCTTACGTAAGAGG
 RGL β 535 AACTACGGACCTGCAGGAAATTTTGCAAATATGCCTCCTTACGTAAGAGG
 consensus 651 AACTACGGACCTGcAGGaAATTTtgCAAAaTatGCCTccTtAcgtaAGAGG

RTVP-1 695 AGCCACCTGCAGTGCCTGCCCCAATAATGACAAGTGTTTGGACAATCTCT
 RGL α 585 AGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAACCTCT
 RGL β 585 AGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAACCTCT
 consensus 701 AGaatCtTGctcTctCTGctCaAAagAaGAgAAaTGtgTaaAgAAcCTCT

RTVP-1 745 GTGTTAACCAGACAGCGAGACCAAGTGAAACGTTACTACTCTGTGTATAT
 RGL α 635 GCA-----AAAATCCATTTCTGAAG
 RGL β 635 GCAGGACTCCACAACCTTATTATACCTAACC---AAAATCCATTTCTGAAG
 consensus 751 Gca a c acagc g a aa c AaaAtcCatTTcTgaAg

RTVP-1 795 CCAGGCTGGCCCATATATCCACGTAACAGATACACTTCTCTCTTTCTCAT
 RGL α 655 CCAACGGGG-----AGAGCACCTCAGCAGACAGCCTTTAATCCAT-TCAG
 RGL β 682 CCAACGGGG-----AGAGCACCTCAGCAGACAGCCTTTAATCCAT-TCAG
 consensus 801 CCAacggGG AgAgCacCtcAgCAGAcAgcCTTtaatCcaT TCAG

RTVP-1 845 TGTTAATTCAGTAATTCTAATACTGTCTGTTATAATTACCATTTTGGTAC
 RGL α 699 CTTAGGTTTCTTCTTCTGAGAAT--CTTTTAATGT---CATTTATATAC
 RGL β 726 CTTAGGTTTCTTCTTCTGAGAAT--CTTTTAATGT---CATTTATATAC
 consensus 851 ctTaggTTttcTtctTCTgAgAaT CTtTTAatgT CATTTataTAC

RTVP-1 895 AGCTCAAGTACCCTAATTTAGTTCTTTTGGACTAATACAATTCAGGAA-A
 RGL α 744 AAAAGAAATTCTCAAATGT-----TAAATAAAGGAATA

RGL β 771 AAAAGAAATTCTCAAATGT-----TAAAATAAAGGAATA
 consensus 901 AaaagAAaTtCtCaAATgT TAAaATaaAGGAAtA

RTVP-1 944 GAAAAAACCCTAAAAACCAACCTCATTACATATGGCTTTTTT--TTAACC
 RGL α 778 GTTTATTGCTTAATATAA--CTTATCATCACTTTGCTTCTTTACTGAATC
 RGL β 805 GTTTATTGCTTAATATAA--CTTATCATCACTTTGCTTCTTTACTGAATC
 consensus 951 GtttAttgCttAAAtAtaA CttATcatCActTtGCTTcTTTactGgAatC

RTVP-1 992 AATAACAATTAGGTGTACTTCTATTTTAAAACATTTTCAGAAAAAAATA

RGL α 826 TTCTACACTCTTGC---CTGATACCTAAA----- (SEQ ID NO: 1)

RGL β 853 TTCTACACTCTTGC---CTGATACCTAA----- (SEQ ID NO: 3)
 consensus1001 ttctACAcTcttGc CTgaTAccTaAA

FIGURE 2**RTVP-1 and RGL1 α , RGL1 β protein compare**

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RTVP-1      MRVTLATIAWMVSFVSNSYSTANILPDIENEDFIKDCVRIHNKFRSEVKPTASDMLYMTW
RGL $\alpha$       MALKNKFSCWLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIW
RGL $\beta$       MALKNKFSCWLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIW
RTVP-1      1
RGL $\alpha$       DPALAQIAKAWASNCQFSHNTRLKPPHKLHPNFTSLGENIWTGSPVIFSVSSAITNWDYDE
RGL $\beta$       DKGLAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNE
RTVP-1      IQDYDFKTRICKKVCGHYTTQVWVADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGN
RGL $\alpha$       TQFYDFDSLSCSRVCGHYTQLVWANSFYVGCAMCPNLGG---ASTAIFVCNYGPAGN
RGL $\beta$       TQFYDFDSLSCSRVCGHYTQLVWANSFYVGCAMCPNLGG---ASTAIFVCNYGPAGN
RTVP-1      YPTW-PYKRGATCSACPNNNDKCLDNLC-----VNRQRDQVK-RYYSVVY
RGL $\alpha$       FANMPPYVRGESCSLCSKEEKCCKVKNLCK-----NPFLKPTGRAPQQTAFNPFSLGF
RGL $\beta$       FANMPPYVRGESCSLCSKEEKCCKVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGF
RTVP      PGWPIYPRNRYTSLFLIVNSVILILSVIITILVQLKYPNLVLLD
RGL $\alpha$       LLLRIF (SEQ ID NO: 2)
RGL $\beta$       LLLRIF (SEQ ID NO: 4)

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signal peptide
 SCP-domain(sig1,sig2)
 Caveolin binding site
 TM-domain

MQVILAVIVWM
 VCGHYTQVWVAD
 YNETQFYDF
 YTSFLIVNSVILILSVIITILV

FIGURE 3

RGL 1 p53 binding sites
(Promoter 4kb--intron 4)

- Intron 1
- 581 AAATAAGTTC AAAACT GTACTAGTCT 90% (A)
- Intron 2
- 1559 AGACTAGTTT CTTAC ATACATGTTT 95% (B)
- 1559 AAGCCTGTTT AAGCAATATAAA GAGCTAACCT
TCTTCTCT AGACTTACCC 90% (C, C2)
- 16403 GAGCTTACTC TTTAT TGGCTAGTTT 90% (D)
- Intron 3
- 3116 AGATAAGTCT GA GGTCTTGCTCT 90% (E)
- 32226 AGACAAGCCA CCTGG AAGAAAGTCT 90% (F)
- Intron 4
- 35786 AAACAAACTT T AGACAAGTTT 95% (G)
- 36649 TAACTAGTTT GGGTACTAGTAAACC
TGGCATGCCC TC AAACTTTTTC 90% (H1, H2)
- 38942 AGACATTCTC TATA AAGCTATTTT 90% (I)

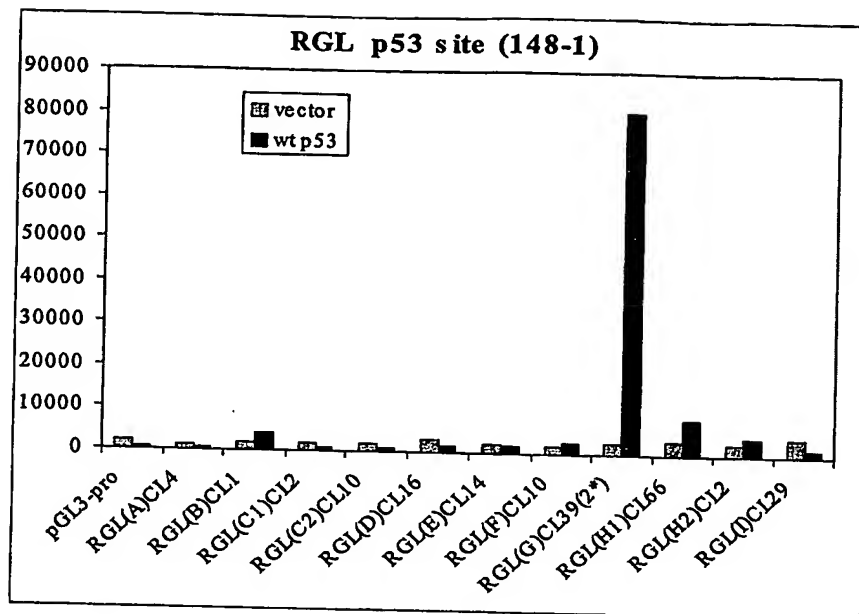
FIGURE 4

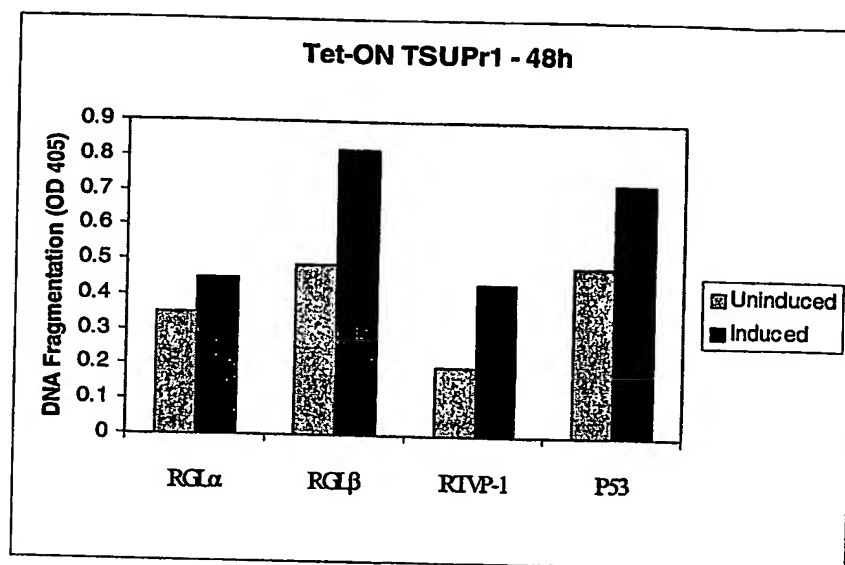
FIGURE 5

FIGURE 6